

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/562,627
Source: IFWP
Date Processed by STIC: 1/10/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/562,627

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 01/10/2006

PATENT APPLICATION: US/10/562,627

TIME: 09:00:14

Input Set : N:\DA\PTO.DA.txt

Output Set: N:\CRF4\01102006\J562627.raw

pp 1-5
Does Not Comply
Corrected Diskette Needed

see item 2 on Enr summary sheet

3 <110> APPLICANT: CHOE, Mu-Hyeon
 4 CHOI, Seong-Hyeok
 5 LEE, Yong-Chan
 6 KWON, Hye-Won
 7 WON, Jae-Seon
 8 YU, Mi-Hyun
 9 SONG, Jeong-Hwa
 10 KIM, Yong-Jae

12 <120> TITLE OF INVENTION: The Dimer of Chimeric Recombinant Binding Domain-Functional Group

13 Fusion formed via Disulfide-bond-bridge and The Process For Producing The Same

15 <130> FILE REFERENCE: 428.1060

C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/562,627

C--> 17 <141> CURRENT FILING DATE: 2005-12-22

17 <150> PRIOR APPLICATION NUMBER: PCT/KR2004/001595

18 <151> PRIOR FILING DATE: 2004-06-30

20 <150> PRIOR APPLICATION NUMBER: KR2003-0043599

21 <151> PRIOR FILING DATE: 2003-06-30

23 <160> NUMBER OF SEQ ID NOS: 12

25 <170> SOFTWARE: KopatentIn 1.71

27 <210> SEQ ID NO: 1

28 <211> LENGTH: 1749

29 <212> TYPE: DNA

30 <213> ORGANISM: PMC74 plasmid coding sequence

32 <400> SEQUENCE: 1

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37	actccagaga agaggctgga gtgggtcgca tacattagta atgatgatag ttccgcccgt	180
39	tattcagaca ctgtaaaggg ccggttcacc atctccagag acaatgccag gaacaccctc	240
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Invalid <213> response see item 10 on Enr summary sheet.

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83 ggccatccgc tgccgctgcg cctggacgcc atcaccggcc ccgaggagga aggcggggcg 1560
85 ctggagacca ttctcggtg gccgctggcc gagcgacccg tggtgattcc ctcggcgatc 1620
87 cccaccgacc cgcgcaacgt cggcgcgac ctcgaccctg ccagcatccc cgacaaggaa 1680
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95 <211> LENGTH: 1764
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97 <213> ORGANISM: PMH21 plasmid coding sequence
98 <400> SEQUENCE: 2
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161 <210> SEQ ID NO: 3
162 <211> LENGTH: 1749
163 <212> TYPE: DNA

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171 actccagaga agaggctgga gtgggtcgca tacattagta atgatgatag ttccgccgct      180
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229 <211> LENGTH: 672
230 <212> TYPE: DNA
231 <213> ORGANISM: pMC75 plasmid coding sequence
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240 ttttctgggg tcccagacag gttcagtggc agtggatcag ggacagattt cacactcaag      240
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343 aacgtcgcg gcgacctcga cccgtccagc atccccgaca aggaacaggc gatcagcgcc      2400
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349 <211> LENGTH: 1233
350 <212> TYPE: DNA

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353 <400> SEQUENCE: 6

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356	cctggagggt	ccctgaaact	ctcctgtgca	acctctggat	tcactttcag	tgactattac	120
358	atgtattggg	ttcgccagac	tccagagaag	aggctggagt	gggtcgcata	cattagtaat	180
360	gatgatagtt	ccgccgctta	ttcagacact	gtaaagggcc	ggttcaccat	ctccagagac	240
362	aatgccagga	acaccctcta	cctgcaaatg	agccgtctga	agtctgagga	cacagccata	300
364	tattcctgtg	caagaggact	ggcctgggga	gcctggtttg	cttactgggg	ccaagggact	360
366	ctggtcactg	tctctgcagc	caaaacgaca	ccccatctg	tctatccact	ggccccctga	420
368	tctgctgccc	aaactaactc	catggtgacc	ctgggatgcc	tggtcaaggg	ctatttccct	480
370	gagccagtga	cagtgcctg	gaactctgga	tccctgtcca	gcggtgtgca	caccttccca	540
372	gctgtcctgc	agtctgacct	ctacactctg	agcagctcag	tgactgtccc	ctccagcacc	600
374	tggcccagcg	agaccgtcac	ctgcaacgtt	gcccacccgg	ccagcagcac	caaggtggac	660
376	aagaaaattg	tgcccagggg	ttgtggtgct	aagccttgca	tagctacaca	agcttccggg	720
378	ggtggcggat	ctggagggtg	cggaagcgga	ggtcccaggg	tgacaggggg	aatggcaagc	780
380	aagtgggatc	agaaggggat	ggacattgcc	tatgaggagg	cggccttagg	ttacaaagag	840
382	ggtggtgttc	ctattggcgg	atgtcttatt	aataacaaag	acggaagtgt	tctcggtcgt	900
384	ggtcacaaca	tgagatttca	aaagggatcc	gccacactac	atggtgagat	ctccactttg	960
386	gaaaactgtg	ggagattaga	gggcaaagt	tacaaagata	ccactttgta	tacgacgctg	1020
388	tctccatgcg	acatgtgtac	aggtgccatc	atcatgtatg	gtattccacg	ctgtgttgct	1080
390	ggtgagaacg	ttaatttcaa	aagtaagggc	gagaaatatt	tacaaactag	aggtcacgag	1140
392	gttgtgtgtg	ttgacgatga	gaggtgtaaa	aagatcatga	aacaatttat	cgatgaaaga	1200
394	cctcaggatt	ggtttgaaga	tattggtgag	tag			1233

397 <210> SEQ ID NO: 7

398 <211> LENGTH: 4871

399 <212> TYPE: DNA

400 <213> ORGANISM: pMC74 plasmid full sequence

402 <400> SEQUENCE: 7

403	taatacgact	cactataggg	agaccacaac	ggtttccctc	tagaaataat	tttgtttaac	60
405	tttaagaagg	agatatacat	atggatgtga	agctggtgga	atctggagga	ggcttagtgc	120
407	agcctggagg	gtccctgaaa	ctctcctgtg	caacctctgg	attcactttc	agtgactatt	180
409	acatgtattg	ggttcgccag	actccagaga	agaggctgga	gtgggtcgca	tacattagta	240
411	atgatgatag	ttccgcccgt	tattcagaca	ctgtaaaagg	ccggttcacc	atctccagag	300
413	acaatgccag	gaacaccctc	tacctgcaaa	tgagccgtct	gaagtctgag	gacacagcca	360
415	tatattcctg	tgcaagagga	ctggcctggg	gagcctgggt	tgcttactgg	ggccaaggga	420
417	ctctggtcac	tgtctctgca	gccaaaacga	cacccccatc	tgtctatcca	ctggcccctg	480
419	gatctgctgc	ccaaactaac	tccatggtga	ccctgggatg	cctggtcaag	ggctatttcc	540
421	ctgagccagt	gacagtgacc	tggaactctg	gatccctgtc	cagcgtgtgt	cacaccttcc	600
423	cagctgtcct	gcagtctgac	ctctacactc	tgagcagctc	agtgactgtc	ccctccagca	660
425	cctggcccag	cgagaccgtc	acctgcaacg	ttgcccaccc	ggccagcagc	accaaggtgg	720
427	acaagaaaat	tgtgcccagg	gattgtggta	gtaagcctag	cataagtaca	aaagcttccg	780
429	gaggtcccga	gggcggcagc	ctggccgcgc	tgaccgcgca	ccaggcttgc	cacctgccgc	840
431	tggagacttt	caccgcgtcat	cgccagccgc	gcggtgggga	acaactggag	cagtgcggct	900
433	atccggtgca	gcggtgggtc	gccctctacc	tggcggcgcg	gctgtcgtgg	aaccaggctg	960
435	accaggatgat	ccgcaacgcc	ctggccagcc	ccggcagcgg	cggcgacctg	ggcgaagcga	1020
437	tccgcgagca	gccggagcag	gcccgtctgg	ccctgaccct	ggccgcgcgc	gagagcgagc	1080
439	gcttcgtccg	gcagggcacc	ggcaacgacg	aggccggcgc	ggccaacggc	ccggcggaca	1140
441	gcggcgacgc	cctgctggag	cgcaactatc	ccactggcgc	ggagttcctc	ggcgacggcg	1200
443	gcgacgtcag	cttcagcacc	cgcggcacgc	agaactggac	ggtggagcgg	ctgctccagg	1260

FYI

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

DATE: 01/10/2006

PATENT APPLICATION: US/10/562,627

TIME: 09:00:15

Input Set : N:\DA\PTO.DA.txt

Output Set: N:\CRF4\01102006\J562627.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date